

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/451,739G

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 X Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



<110> Jager, Dirk
Scanlan, Matthew
Gure, Ali
Jager, Elke
Knuth, Alexander
Old, Lloyd
Chen, Yao-tseng

<120> Isolated Nucleic Acid Molecules Encoding Cancer Associated Antigens,
the Antigens per se, and Uses Thereof

<130> LUD 5615

<140> 09/451,739

<141> 1999-11-30

<160> 12

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 Ala Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg
 65 70 75 80
 Ser Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val
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 Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu
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Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val Gly Ala Asp Arg
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Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro Asn Ser Lys Arg
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Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys Ala Glu Arg Glu
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Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu Pro Thr Tyr Cys
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Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly Cys Asp Asn Asp
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Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val Gly Leu Asn His
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Ser Gln Met Val Glu Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser
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His Val Glu Leu Phe Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly
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Asn Ser Gly Lys Val Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala
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Gln Ser Asp Lys Pro Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn
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Glu Asn Arg Glu Asn Ala Ser Ser Asn His Asp His Asp Asp Gly Ala
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180 185 190

His Phe Ser Cys Val Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr
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Lys	Asp	Tyr	Glu	Glu	Ser	Ser	Trp	Asp	Ser	Glu	Ser	Leu	Cys	Glu	Thr
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		210				215					220				
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225					230					235					240
Arg	Ala	Arg	Glu	Leu	Gln	Lys	Asp	His	Cys	Glu	Gln	Arg	Thr	Gly	Lys
				245					250					255	
Met	Glu	Gln	Met	Lys	Lys	Lys	Phe	Cys	Val	Leu	Lys	Lys	Lys	Leu	Ser

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275	280	285
Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu		
290	295	300
Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu		
305	310	315
Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln		
325	330	335
Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu		
340	345	350
Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu		
355	360	365
Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu		
370	375	380
Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr		
385	390	395
Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met		
405	410	415
Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr		
420	425	430
Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser		
435	440	445
Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu		
450	455	460
Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile		
465	470	475
Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp		
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Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile		
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 35 40 45
 Leu Thr Arg Gly Trp Gly Arg Ala Trp Pro Trp Lys Gln Ile Leu Lys
 50 55 60
 Glu Leu Asp Glu Cys Tyr Glu Arg Phe Ser Arg Glu Thr Asp Gly Ala
 65 70 75 80
 Gln Lys Arg Arg Met Leu His Cys Val Gln Arg Ala Leu Ile Arg Ser
 85 90 95
 Gln Glu Leu Gly Asp Glu Lys Ile Gln Ile Val Ser Gln Met Val Glu
 100 105 110
 Leu Val Glu Asn Arg Thr Arg Gln Val Asp Ser His Val Glu Leu Phe
 115 120 125
 Glu Ala Gln Gln Glu Leu Gly Asp Thr Val Gly Asn Ser Gly Lys Val
 130 135 140
 Gly Ala Asp Arg Pro Asn Gly Asp Ala Val Ala Gln Ser Asp Lys Pro
 145 150 155 160
 Asn Ser Lys Arg Ser Arg Arg Gln Arg Asn Asn Glu Asn Arg Glu Asn
 165 170 175
 Ala Ser Ser Asn His Asp His Asp Asp Gly Ala Ser Gly Thr Pro Lys
 180 185 190
 Glu Lys Lys Ala Lys Thr Ser Lys Lys Lys Lys Arg Ser Lys Ala Lys
 195 200 205
 Ala Glu Arg Glu Ala Ser Pro Ala Asp Leu Pro Ile Asp Pro Asn Glu
 210 215 220
 Pro Thr Tyr Cys Leu Cys Asn Gln Val Ser Tyr Gly Glu Met Ile Gly
 225 230 235 240
 Cys Asp Asn Asp Glu Cys Pro Ile Glu Trp Phe His Phe Ser Cys Val
 245 250 255
 Gly Leu Asn His Lys Pro Lys Gly Lys Trp Tyr Cys Pro Lys Cys Arg
 260 265 270
 Gly Glu Asn Glu Lys Thr Met Asp Lys Ala Leu Glu Lys Ser Lys Lys
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 Glu Arg Ala Tyr Asn Arg
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